Amendments To The Specification:

Please amend the title on page i of the Table of Contents and on page 1 of the Specification as follows:

~~GENE DISCOVERY USING MICROARRAYS~~ POSITIONALLY-ADDRESSABLE ORDERED POLYNUCLEOTIDE ARRAYS

Please amend the paragraph beginning on page 8, line 13 of the specification, as follows:

~~FIG. 14 depicts~~ FIGS. 14A-D depict the characterization of a novel testis transcript using scanning arrays. An Expression Verified Gene (EVG; see Example 5) discovered in the analysis of chromosome 22 was localized to a 10 kb region at one end of the insert of BAC clone AL031587 (FIG. 14A). Following the described method, both strands of this 113 kb genomic interval were tiled with 60mer probes placed in 10bp intervals. The scanning array was hybridized with RNA isolated from human testis (FIG. 14B). Hybridization signals corresponding to scanning probes from this region were filtered and plotted as $\log_{10}$ values of the normalized signal strengths. Detailed views of scanning data showing one correctly predicted exon and one incorrectly predicted exon are shown in FIG. 14C. After narrowing the search window for a given intron/exon boundary down to a 20-30 bp region using scanning data, the exact splice junction was then identified using a combination of consensus sequences (GT-AG rule) and ORF information. FIG. 14D presents the sequence of a segment of chromosome 22 DNA (SEQ ID NO: 1) containing the 3' end of an intron (left), the "AG" splice site signal, and the 5' end of the sequence of exon 3.

Please amend the paragraph beginning on page 38, line 13 of the specification as follows:

Target polynucleotides were obtained by preparing total RNA from two cell lines, a human T lymphocyte cell line (Jurkat, ATCC # TIB-152) and a chronic myelogenous leukemia cell line (K562, ATCC #CCL-243), as described previously (Marton *et al.*, 1998, *Nat. Med.* 4:1293-1301). Poly-A+ RNA (mRNA) was isolated from each cell line and labeled using reverse transcription primed with a mixture of random 9-mers and d(T)-20 primers. Specifically, 1.5 μg of mRNA was mixed with 1.5 μg of random 9-mers and 1.5 μg of d(T)-20, and the mixture was incubated for 10 minutes at 70°C, 10 minutes at 4°C, and 10 minutes at 22°C. To this mixture was added 0.5 mM amino-allyl –dUTP (Sigma A-0410), 0.5 mM dNTP, 1xRT buffer, 5 mM $MgCl_2$, 10 mM DTT, and 200 units Superscript

(GibcoBRL), bringing the final reverse transcription reaction volume to 100 µl. This reverse transcription reaction was incubated for 10 minutes at 42°C, then the RNA was hydrolyzed by adding 20 µl EDTA+NaOH and incubating at 65°C for 20 minutes. The reaction was neutralized by adding 20 µl of 1 M Tris-HCl pH 7.6. The resulting amino-allyl labeled single-stranded cDNA was purified using a Microcon-30 (Millipore, Bedford, Mass.). The purified cDNA resulting from the Jurkat cells was coupled to Cy3 dye using a ~~Cy Dye™~~ CYE DYE™ labeling kit (Amersham Pharmacia, Piscataway, N.J., #Q15108), while the purified cDNA resulting from the K562 cells was coupled to Cy5 dye in the same manner.

Please amend the paragraph beginning on page 40, line 3 of the specification as follows:

Target polynucleotides were obtained by preparing total RNA from two cell lines, Jurkat (ATCC # TIB-152) and K562 (ATCC #CCL-243), as described in Example 1. Poly-A+ RNA (mRNA) was isolated from each cell line and labeled using reverse transcription primed with a mixture of random 9-mers and d(T)-20 primers. Specifically, 1.5 µg of mRNA was mixed with 1.0 µg of random 9-mers and 2.5 µg of d(T)-20, and the mixture was incubated for 10 minutes at 70°C, 10 minutes at 4°C, and 10 minutes at 22°C. To this mixture was added 0.5 mM amino-allyl –dUTP (Sigma A-0410), 0.5 mM dNTP, 1xRT buffer, 5 mM $MgCl_2$, 10mM DTT, and 200 units Superscript (GibcoBRL), bringing the final reverse transcription reaction volume to 100 µl. This reverse transcription reaction was incubated for 10 minutes at 42°C, then the RNA was hydrolyzed by adding 20 µl EDTA+NaOH and incubating at 65°C for 20 minutes. The reaction was neutralized by adding 20 µl of 1 M Tris-HCl pH 7.6. The resulting amino-allyl labeled single-stranded cDNA was purified using a Microcon-30 (Millipore, Bedford, Mass.). The purified cDNA resulting from the Jurkat cells was coupled to Cy5 dye using a ~~Cy Dye™~~ CYE DYE™ labeling kit (Amersham Pharmacia, Piscataway, N.J., #Q15108), while the purified cDNA resulting from the K562 cells was coupled to Cy3 dye in the same manner.

Please amend the paragraph beginning on page 43, line 32 of the specification as follows:

For a single hybridization, 1.5 µg of mRNA was combined with 1.0 µg of random 9-mers and the mixture was incubated for 10 minutes at 70°C, 5 minutes at 4°C, and 10 minutes at 22°C. To this mixture was added 0.5 mM amino-allyl dUTP (Sigma A-0410), 0.5 mM dNTP, 1xRT buffer, 5 mM $MgCl_2$, 10 mMDTT, and 200 units Superscript (GibcoBRL),

bringing the final reverse transcription reaction volume to 400 µl. This reverse transcription reaction was incubated for 20 minutes at 42°C then the RNA was hydrolyzed by adding 20 µl EDTA+NaOH and incubating at 65°C for 20 minutes. The reaction was neutralized by adding 20 ul of 1M Tris-HCl pH 7.6. The resulting amino-allyl labeled single-stranded cDNA was purified using a Microcon-30 (Millipore, Bedford, MA). The purified cDNA was coupled to either Cy3 or Cy5 dye using a ~~Cy Dye™~~ CYE DYE™ labeling kit (Amersham Pharmacia, Piscataway, NJ, #Q15108). The dye incorporation and total cDNA were determined spectrophotometrically. Hybridization to the array was carried out as described in Example 1.